## **Resource Summary Report**

Generated by NIF on Apr 28, 2025

# **ChIPsim**

RRID:SCR\_001293 Type: Tool

**Proper Citation** 

ChIPsim (RRID:SCR\_001293)

#### **Resource Information**

URL: http://www.bioconductor.org/packages/release/bioc/html/ChIPsim.html

Proper Citation: ChIPsim (RRID:SCR\_001293)

**Description:** Software package providing a general framework for the simulation of ChIPseq data. Although currently focused on nucleosome positioning the package is designed to support different types of experiments.

Abbreviations: ChIPsim

Synonyms: ChIPsim - Simulation of ChIP-seq experiments

Resource Type: software resource

Keywords: chip-seq, infrastructure, simulation

Funding:

Availability: GNU General Public License, v2 or newer

Resource Name: ChIPsim

Resource ID: SCR\_001293

Alternate IDs: OMICS\_02042

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014025+0000

### **Ratings and Alerts**

No rating or validation information has been found for ChIPsim.

No alerts have been found for ChIPsim.

#### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Thomas R, et al. (2017) Features that define the best ChIP-seq peak calling algorithms. Briefings in bioinformatics, 18(3), 441.